

Thu Mar 24 08:02:13 2005

us-10-6

Db	234	QIHVSFONCVNVQASNLMTAPENSPNTDGIHVTGTQNIHIISSCVIGTGDDCISIVNGSR	293
Qy	281	NVQATNITCGPGHGISISGLSGNSEAVSVNVTVEAKIIGAENGVRITKWGGSGOASN	340
Db	294	KVRVNDITCGPGHGISISGLSGNSEAHVSDVVVNGAKLCGTTNGVRITKWGGSGOASN	353
Qy	341	IKFLNVMQDVKYPIIIDQNYCDRVEPCIQQFSVQVKNVYVENIKGTSATKYAIKFDCS	400
Db	354	IKFQVNMHVNPPIIIDQNYCDQDKPCQEQSSAVQVKNVYQNIKGTCSNVAITFDCS	413
Qy	401	TNFPCEGIIMENINLVSGSKPSEATCKNVHFNNAEHVTPHCTSLSEISE	451
Db	414	KRFPQGVLEVDVLEIEGGAALKCNVELSETGVVSPHCQEGGEE	464

PGLR\_ACTCH STANDARD; PRT; 467 AA.

AC P35336;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).

OS Actinidia chinensis (Kiwi) (Yangtao).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Ericales; Actinidiaceae; Actinidia.

OX NCBI\_TaxID=3625;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Deliciosa;

RX MEDLINE=94302157; PubMed=8029342; DOI=10.1104/pp.103.2.669;

RA Atkinson R.G., Gardner R.C.;

RT "A polygalacturonase gene from kiwifruit (*Actinidia deliciosa*).";

RL Plant Physiol. 103:669-670(1993).

CC -!- FUNCTION: Acts in concert with the pectinesterase, in the ripening process. Is involved in cell wall metabolism, specifically in polyuronide degradation.

CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DEVELOPMENTAL STAGE: In ripening fruit.

CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 28 family.

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DR EMBL; L12019; AAC14453.1; -

DR InterPro; IPR000743; Glyco\_hydro\_28.

DR InterPro; IPR006626; PbH1.

DR InterPro; IPR011050; Pectin lyas like.

DR Pfam; PF00295; Glyco\_hydro\_28; 1.

DR SMART; SM00710; PbH1; 4.

DR PROSITE; PS00502; POLYGALACTURONASE; 1.

KW Cell wall; Fruit ripening; Glycoprotein; Glycosidase; Hydrolase;

KW Signal.

FT SIGNAL 1 27 Potential.

FT CHAIN 28 467 Polygalacturonase.

FT ACT\_SITE 306 306 Probable.

FT CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 467 AA; 50776 MW; 5A9A61483C028B7A CRC64;

Query Match 54.2%; Score 1295.5; DB 1; Length 467;

Best Local Similarity 54.8%; Pred. No. 2e-82;

Matches 257; Conservative 75; Mismatches 112; Indels 27; Gaps 7;

QY 1 MVIQRN--STLLIIIFASSISITCRSNVDDNLFKQVYDNLBOEFAHDFQAVLSYLSKN 58

DB 1 MALQREFFQFVITLLIPSLFGYTSVHED----PPHYHLE-EYGYDFRAFPSYITTI 55

QY 59 IESNNIDKVDKNGI-----KVINVLSFGAKGDKTYDNIAPFQAWNE 101

DB 56 GONDGSSMSHENGIFGLRKVDYGMDRVLDASKTVNVDDFGAKGDRD-DTKAFERAWKA 114

QY 102 ACSSTRPVQVVPKKNYLLKQITFSGPCRSISVKIFGSLSEASSKISDY-KORRLWIAF 160

DB 115 ACSSTSSAVLLVPK-KNYLVRPIFSFGCKSGLTMQIYGTIEASDDRSYRKDGRHWLVF 173

QY 161 DSVQNLVGGGGTNGNGVWPPSSCKINKSLPCRDPATLTFWNCNKLKVNLSKNAQ 220

DB 174 DSVQNLRVGGGTNGNGKHWQNSCKTNKALPCKDAPALTLYKSHVIVKLNKLENAQ 233

QY 221 QIHKFESCTNVVASNLMINASAKSPNTDGVHVSNTQYIQISDTIIGTGDCCISIVSGSQ 280